
*** TX REPORT ***

TRANSMISSION OK

TX/RX NO	1040	
CONNECTION TEL		912123183400
SUBADDRESS		
CONNECTION ID		
ST. TIME	09/15 20:26	
USAGE T	05'55	
PGS.	9	
RESULT	OK	

Crystal Mall 1, 7th Floor
1911 South Clark Street
Arlington, VA 22202
Tel.: 703-308-8362
Fax: 703-746-5195

USPTO

Fax

To: Norman Hanson

From: Examiner Canella

Fax: 212-318-3400

Pages: 9, inclusive

Phone:

Date: 9/15/03

Re: 09/270,437

CC:

☐ **Urgent** ☐ **For Review** ☐ **Please Comment** ☐ **Please Reply** ☐ **Please Recycle**

● **Comments:**

Copies of the attachment to 09/270,437. I apologize for the omission.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

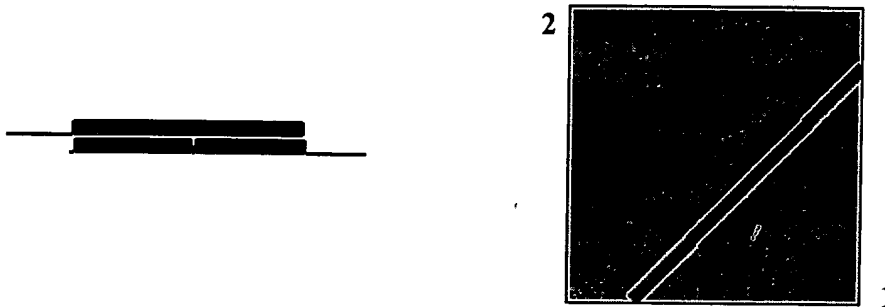
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:5

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lc|seq_1 Length 577 (1 .. 577)

Sequence 2 lc|seq_2 Length 1708 (1 .. 1708)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 854 bits (2206), Expect = 0.0

Identities = 438/445 (98%), Positives = 439/445 (98%)

Frame = +2

```
Query: 133 RQAIMKLNQHLENHALKVSYPDEQITQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 192
          R AIMKLNQHLENHALKVSYPDEQI QGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ
Sbjct: 32  RQAIMKLNQHLENHALKVSYPDEQIAQGPENGRGGFGSRGQPRQGSPPVAAGAPAKQQ 211

Query: 193 PVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252
          VDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG
Sbjct: 212 QVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391

Query: 253 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRNLKKVEQDTETKITI 312
          CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRNLKKVEQDTETKITI
Sbjct: 392 CSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRIGKEGRNLKKVEQDTETKITI 571

Query: 313 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAA 372
          SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAA
Sbjct: 572 SSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS --SHLIPGLNLAA 745

Query: 373 VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 432
          VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS
Sbjct: 746 VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLS 925

Query: 433 RFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHI 492
          RFASASIKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHI
Sbjct: 926 RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHI 1105

Query: 493 RVPASAAGRVIGGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 552
          RVPASAAGRVIGGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK
```

Sbjct: 1106RVPASAAGRVIGGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK 1285

Query: 553 IRDILAQVKQQHQKQGSNLAQARRK 577
IRDILAQVKQQHQKQGSN AQARRK

Sbjct: 1286IRDILAQVKQQHQKQGSNQAQARRK 1360

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 11,732

Number of Sequences: 0

Number of extensions: 7631

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

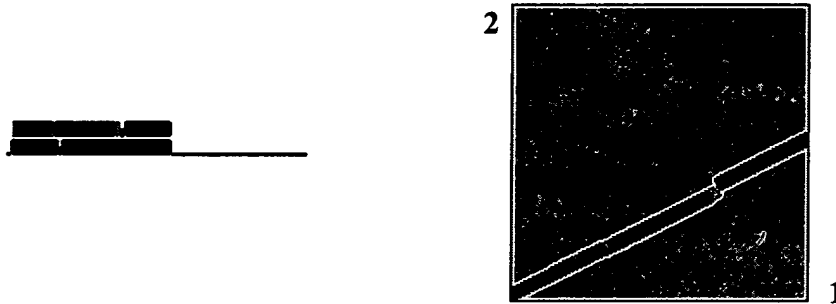
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:6

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 3412 (1 .. 3412)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 775 bits (2000), Expect = 0.0
 Identities = 394/603 (65%), Positives = 476/603 (78%), Gaps = 26/603 (4%)
 Frame = +1

```

Query: 1  MNKLYIGNLNESVTPADLEKVF AEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFS GK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIETLSGK 252

Query: 61  VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTESETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTDTETA 432

Query: 121  VVNVTYSNREQTRQAIMKLNHGHQLENHALKVSYPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRLLVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENS G 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADDEVPLKILAHNNFVGRGLIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGRGLIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAEIPLKILAHNGLVGRGLIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T KITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDL SIYNPERTITVKGTV EACASAEI EIMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAVGLFPASSSAVPPP--PSSVTGAAPYSSFM----- 400
          + Q++LIPGLNL+A+G+F S + PP P AAPY F
  
```

Sbjct: 1138NQANLIPGLNLSALGIFSTGLSVLSPPAGPRGAPPAAPYHPFTTHSGYFSSLYPHHQFG 1317

Query: 401 -----QAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMV 454
PEQE+V +FIP QAVGAIIGKKG HIKQL+RFA ASIKIAP E PD RMV

Sbjct: 1318PFPHHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSEVMV 1497

Query: 455 VITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQ 514
+ITGPPEAQFKAQGRI+GKLKEENFF PKKEEVKLE HIRVP+S AGRVIGKGGKTVNELQ

Sbjct: 1498IITGPPEAQFKAQGRIFGKLKEENFFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQ 1677

Query: 515 NLTAAEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRKIRDILAQVKQHQKQSNLAQA 574
NLT+AEV+VPRDQTPDEN++VIV+IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A

Sbjct: 1678NL TSAEVIVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQ 1857

Query: 575 RRK 577

R K

Sbjct: 1858RSK 1866

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 21,798

Number of Sequences: 0

Number of extensions: 14808

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

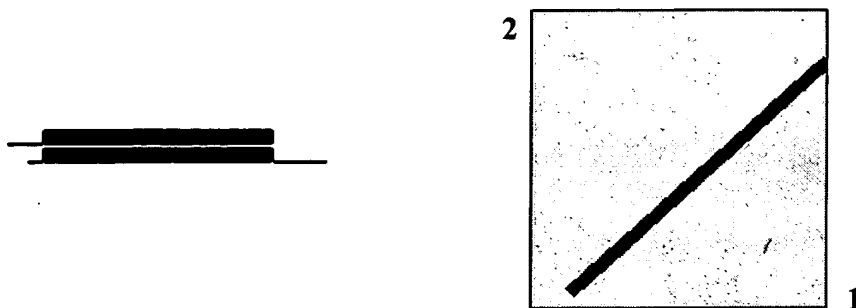
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:7

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 1946 (1 .. 1946)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 963 bits (2489), Expect = 0.0
 Identities = 493/499 (98%), Positives = 494/499 (98%)
 Frame = +3

```

Query: 79  RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTESETA VVNVTYSNREQTRQAIMK 138
          RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTESETA VVNVTYSNREQTRQAIMK
Sbjct: 108 RSRKIQIRNIPPQLRWEVLDSLLAQYGTVENCEQVNTESETA VVNVTYSNREQTRQAIMK 287

Query: 139 LNQHLENHALKVSYPDEQITQGPENGRRGFGSRGQPRQGSPVAAGAPAKQQPVDIPL 198
          LNQHLENHALKVSYPDEQI QGPENGRRGFGSRGQPRQGSPVAAGAPAKQQ VDIPL
Sbjct: 288 LNQHLENHALKVSYPDEQIAQGPENGRRGFGSRGQPRQGSPVAAGAPAKQQQVDIPL 467

Query: 199 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK 258
          RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK
Sbjct: 468 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGCSSACK 647

Query: 259 MILEIMHKEAKDTKTADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL 318
          MILEIMHKEAKDTKTADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL
Sbjct: 648 MILEIMHKEAKDTKTADEVPLKILAHNNFVGRLIGKEGRNLKKVEQDTETKITISSLQDL 827

Query: 319 TLYNPRTITIVKGAIENCCRAEQEIMKKVREAYENDVAAMSLSHLIPGLNLAAVGLFPA 378
          TLYNPRTITIVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAAVGLFPA
Sbjct: 828 TLYNPRTITIVKGAIENCCRAEQEIMKKVREAYENDVAAMS --SHLIPGLNLAAVGLFPA 1001

Query: 379 SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 438
          SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS
Sbjct: 1002SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASAS 1181

Query: 439 IKIAPPETPDSKVRMVVITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA 498
          IKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKKEEVKLETHIRVPASA
  
```

Sbjct: 1182IKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGLKEENFFGPKEEVKLETHIRVPASA 1361

Query: 499 AGRVIGKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 558
AGRVIGKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA

Sbjct: 1362AGRVIGKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILA 1541

Query: 559 QVKQQHQKGQSNLAQARRK 577
QVKQQHQKGQSN AQARRK

Sbjct: 1542QVKQQHQKGQSNQAQARRK 1598

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 13,365

Number of Sequences: 0

Number of extensions: 8706

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

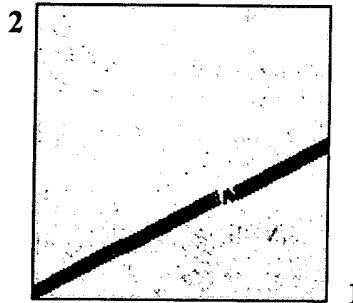
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:8

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 3283 (1 .. 3283)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 742 bits (1916), Expect = 0.0
 Identities = 381/579 (65%), Positives = 458/579 (78%), Gaps = 2/579 (0%)
 Frame = +1

```

Query: 1  MNKLYIGNLNESVTPADLEKVF AEHKISYSGQFLVKSGYAFVDCPDEHWAMKA IETFSGK 60
          MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73  MNKLYIGNLSPAVTADDLRQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAI RAIETLSGK 252

Query: 61  VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLD SLLAQYGTVENCEQVNT ESETA 120
          VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253  VELHGKIMEVDYSVSKLRSRKIQIRNIPP H LQWEVLDGLLAQYGTVENVEQVNTDTET A 432

Query: 121  VVNVTYSNREQTRQAIMKLNQHLENHALKVSYIPDEQITQG--PENGRRGGFGSRGQPR 178
          VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433  VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPPPQRAQRGDHSSREQGH 612

Query: 179  QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAG 238
          A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613  -----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQSRVDIHRKENS G 777

Query: 239  AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTAD E VPLKILAHNNFVGR LIGKEGRN 298
          AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHN VGR LIGKEGRN
Sbjct: 778  AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAE EIPLKILAHNGLVGR LIGKEGRN 957

Query: 299  LKKVEQDTETKITISSLQDLTLYNPRTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
          LKK+E +T TKITISSLQDL++YNPRTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958  LKKIEHETGTKITISSLQDLSIYNPRTITVKG TVEACASAEIEIMKKLREAFENDMLAV 1137

Query: 359  SLQSHLIPGLNLAAVGLFPASSAVPPPPSSVTGAAPYSSFMQAP EQEMVQVFIPAQAVG 418
          + S G F SS P P+ PEQE+V +FIP QAVG
  
```

Sbjct: 1138NTHS-----GYF---SSLYPHHQFG-----PFPHHSYPEQEIVNLFIPTQAVG 1260

Query: 419 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEEN 478
AIIGKKG HIKQL+RFA ASIKIAP E PD RMV+ITGPPEAQFKAQGRI+GKLKEEN

Sbjct: 1261AIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVITGPPEAQFKAQGRIFGKLKEEN 1440

Query: 479 FFGPKKEEVKLETHIRVPASAAGRVIGKGGKTVNELQNLTAAEVVVPRDQTPDENDQVIVK 538
FF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQNLTA+AEV+VPRDQTPDEN++VIV+

Sbjct: 1441FFNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNLTA+AEVIVPRDQTPDENEEVIVR 1620

Query: 539 IIGHFYASQMAQRKIRDILAQVKQQHQKQSNLAQARRK 577

IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A R K

Sbjct: 1621IIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQRSK 1737

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 20,909

Number of Sequences: 0

Number of extensions: 14230

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)